

RESULT 1  
 AAY06483  
 ID AAY06483 standard; Protein; 455 AA.  
 XX  
 AC AAY06483;  
 XX  
 DT 27-SEP-1999 (first entry)  
 XX  
 DE Human tumour-associated protein PRO347.  
 XX  
 KW PRO347; UNQ306; cancer; tumour; diagnosis; therapy; human.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..26  
 FT /note= "signal peptide"  
 FT Protein 27..455  
 FT /note= "mature protein"  
 FT Modified-site 144  
 FT /note= "N-glycosylated"  
 FT Domain 247..279  
 FT /note= "EGF-like domain cysteine pattern signature"  
 FT Domain 280..416  
 FT /note= "EGF-like domain cysteine pattern signature"  
 FT Domain 416..455  
 FT /note= "C-type lectin domain signature"  
 XX  
 PN W09935170-A2.  
 XX  
 PD 15-JUL-1999.  
 XX  
 PF 05-JAN-1999; 99WO-US00106.  
 XX  
 PR 20-NOV-1998; 98US-0109304.  
 PR 05-JAN-1998; 98US-0070440.  
 PR 29-APR-1998; 98US-0083500.  
 PR 22-MAY-1998; 98US-0086414.  
 PR 10-JUN-1998; 98US-0088742.  
 PR 10-NOV-1998; 98US-0107783.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA;  
 PI Roy MA, Wood WI;  
 XX  
 DR WPI; 1999-430385/36.  
 DR N-PSDB; AAX87260.  
 XX  
 PT Antibody against proteins expressed in neoplastic cells, useful for  
 PT tumor diagnosis and treatment  
 XX  
 PS Example 1; Fig 14; 162pp; English.  
 XX  
 CC This sequence represents human PRO347 (UNQ306), a 50.5 5 kDa protein  
 CC (PI 8.44) encoded by the novel cDNA clone DNA44176 (see AAX87260).  
 CC Amplification of DNA44176 was observed in various tumour lines,  
 CC suggesting a role in tumour formation and growth. Antagonists  
 CC (e.g. antibodies) directed to PRO347 may have use in cancer therapy.  
 CC The invention identifies 14 genes (see AAX87254-67) that are amplified  
 CC in the genome of tumour cells. Such amplification is expected to be  
 CC associated with overexpression of the gene product and to contribute  
 CC to tumorigenesis. The encoded proteins (see AAY06477-90) may be  
 CC useful targets for the diagnosis and/or treatment (including  
 CC prevention) of certain cancers, and may act as predictors of the  
 CC prognosis of tumour treatment. Antibodies that bind the proteins  
 CC are claimed and used in claimed cancer diagnostic kits.  
 XX  
 SQ Sequence 455 AA;

Query Match 100.0%; Score 2529; DB 20; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-183;  
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLHPETSPGRGHLLAVILLALLGTTWAEVWPPQQLQEQAPMAGALNRKESFLLSLHNRLRS 60  
 |||||||  
 Db 1 MLHPETSPGRGHLLAVILLALLGTTWAEVWPPQQLQEQAPMAGALNRKESFLLSLHNRLRS 60

Qy 61 WVQPPAADMRRLDWSDSLALQALQARAALCGIPTPSLASGLWRQLQVGWNMQLLPAGLASF 120  
 |||||||  
 Db 61 WVQPPAADMRRLDWSDSLALQALQARAALCGIPTPSLASGLWRQLQVGWNMQLLPAGLASF 120

Qy 121 VEVVSLWFAEGQRYSHAAEGCARNATCTHYTQLVWATSSQLGCGRHLCAGQTAIEAFVC 180  
 |||||||  
 Db 121 VEVVSLWFAEGQRYSHAAEGCARNATCTHYTQLVWATSSQLGCGRHLCAGQTAIEAFVC 180

Qy 181 AYSPGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCONHG 240  
 |||||||  
 Db 181 AYSPGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCONHG 240

Qy 241 RLNISTCHCHCPCPGYTGRYCVQRCSSLQCVHGRFREEECSCVCDIGYGGACATKVHFFH 300  
 |||||||  
 Db 241 RLNISTCHCHCPCPGYTGRYCVQRCSSLQCVHGRFREEECSCVCDIGYGGACATKVHFFH 300

Qy 301 TCDLRIDGDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLRLETTNEVT 360  
 |||||||  
 Db 301 TCDLRIDGDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLRLETTNEVT 360

Qy 361 DSDFETRNFWIGLTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVEL 420  
 |||||||  
 Db 361 DSDFETRNFWIGLTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVEL 420

Qy 421 QASAAFNWNDQRCKTRNRYICQFAQEHEISRWGPGS 455  
 |||||||  
 Db 421 QASAAFNWNDQRCKTRNRYICQFAQEHEISRWGPGS 455

*Sequence  
Claims*

RESULT 4  
 ID AAY41266 standard; Protein; 446 aa.  
 XX  
 AC AAY41266;  
 XX  
 DT 31-JAN-2000 (first entry)  
 XX  
 DE Human T139 protein.  
 XX  
 KW Human; T139 polypeptide; immune system disorder; spermatogenesis;  
 sperm-egg fusion; testicular disorder; testicular cancer; gene mapping.  
 OS Homo sapiens.  
 XX  
 MC09954343-A2.  
 XX  
 28-OCT-1999.  
 XX  
 PR 23-APR-1999; 99WO-US08896.  
 XX  
 DR WPI; 1999-633969/54.  
 XX  
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
 XX  
 PT Holtzman D;  
 XX  
 DR N-PSDB; AA223299; AA223300.  
 XX  
 PT Human T139 nucleic acids and polypeptides, useful for treating or  
 proliferative disorders associated with aberrant T139 expression or  
 activity.  
 XX  
 PS Claim 9; Fig 1; 115pp; English.  
 XX  
 CC This represents a human T139 Polypeptide. The T139 polypeptide can be  
 expressed by standard recombinant methodology. The T139 cDNA insert is  
 deposited with ATCC under accession number 98694. The T139 polypeptides  
 and polynucleotides can be administered therapeutically or  
 prophylactically to treat/prevent disorders associated with aberrant T139  
 expression or activity, especially proliferative or differentiative  
 disorders, e.g. of the immune system. They can be used to modulate  
 spermatogenesis, e.g. as a contraceptive to decrease spermatogenesis or  
 to treat disorders related to defects in sperm-egg fusion. They may also  
 be useful to treat testicular disorders, e.g. testicular cancer. The  
 polypeptides may be used to identify selectively binding compounds which  
 may be useful for detecting the polypeptides in samples; and identifying  
 compounds modulating polypeptide activity. The polynucleotides are useful  
 for producing probes or primers that selectively hybridize to the  
 polynucleotides which may be useful for detecting the polynucleotides in  
 a sample, gene mapping; identifying cells or tissues expressing aberrant  
 T139 levels; determining if a gene has been mutated or deleted to  
 identify subjects at risk for or having a disorder associated with T139  
 expression or activity and to monitor therapeutic interventions; and for  
 producing antisense sequences for therapeutic administration to modulate  
 T139 expression.  
 XX  
 SQ Sequence 446 AA;

Query Match 96.8%; Score 2447.5; DB 20; Length 446;  
 Best Local Similarity 97.1%; Pred. No. 2, 4e-177;  
 Matches 422; Conservative 1; Mismatches 3; Indels 9; Gaps 1;

QY 1 MLAPETSPGRGHLLAVLIALIGSTWAIWPPQLEQPMAGALNKRKESPLLSLNRLRS 60  
 1 MLHPETSPGRGHLLAVLIALLGTLAWEVWPPQLEQPMAGALNKRKESPLLSLNRLRS 60

QY 61 WTOPPADMRLWDSDLSLAQALQARALCGIPTSLASLGIWRTLQGRNMQMLLPAGLASF 120  
 Db 61 WTOPPADMRLWDSDLSLAQALQARALCGIPTSLASLGIWRTLQGRNMQMLLPAGLASF 120  
 QY 121 VEVVSLNPAEGORYSHAGEARNATCTHTQLYWATSSQIGGRHLCSAGQQAIEAVC 180  
 Db 121 VEVVSLNPAEGORYSHAGEARNATCTHTQLYWATSSQIGGRHLCSAGQQAIEAVC 180  
 QY 181 AKSPFGNNEVNGKTIPIYKGAWCCTASVSGCFKAWDHAGGLECPVRNPCRMSQHNG 240  
 Db 181 AKSPFGNNEVNGKTIPIYKGAWCCTASVSGCFKAWDHAGGLECPVRNPCRMSQHNG 240  
 QY 241 RLNTSTCHCCHCPGTYCQVRCSTLQVHGRFREECSCVCDITYGGNQCATKWHFPPH 300  
 Db 241 RLNTSTCHCCHCPGTYCQVRCSTLQVHGRFREECSCVCDITYGGNQCATKWHFPPH 300  
 QY 301 TCDLRIDDCFMSSADTYTARMKQKGVLQIKSKYDIAFLAFGRLENTNEV 360  
 Db 301 TCDLRIDDCFMSSADTYTARMKQKGVLQIKSKYDIAFLAFGRLENTNEV 360  
 QY 361 DSDFTRNEWIGLTYKTAKDSFRWATGEHQARTSFAGQPDNH-----GRNCVEL 411  
 Db 361 DSDFTRNEWIGLTYKTAKDSFRWATGEHQARTSFAGQPDNH-----GRNCVEL 411  
 QY 421 QASAFNWNQDQRKTRNRYICQFAEHISRMWPGS 455  
 Db 421 QASAFNWNQDQRKTRNRYICQFAEHISRMWPGS 455  
 QY 412 QASAFNWNQDQRKTRNRYICQFAEHISRMWPGS 446  
 Db 412 QASAFNWNQDQRKTRNRYICQFAEHISRMWPGS 446